

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/553,160
Source: IFWO
Date Processed by STIC: 05/09/2006

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IFWO

RAW SEQUENCE LISTING

DATE: 05/09/2006

PATENT APPLICATION: US/10/553,160

TIME: 09:42:16

Input Set : A:\A-71973.ST25.txt

Output Set: N:\CRF4\05092006\J553160.raw

3 <110> APPLICANT: Mount Sinai School of Medicine of New York University
 4 Horvath, Curt
 5 Rodriguez, Jason
 6 Ulane, Christina Marie
 7 Parisien, Jean-Patrick
 9 <120> TITLE OF INVENTION: Methods and Compositions for Inhibiting STAT Signaling

Pathways

11 <130> FILE REFERENCE: 28610/US/2 (461089-00071)
 13 <140> CURRENT APPLICATION NUMBER: US 10/553,160
 14 <141> CURRENT FILING DATE: 2005-10-14
 16 <150> PRIOR APPLICATION NUMBER: PCT/US04/12066
 17 <151> PRIOR FILING DATE: 2004-04-19
 19 <150> PRIOR APPLICATION NUMBER: US 60/463,764
 20 <151> PRIOR FILING DATE: 2003-04-17
 22 <160> NUMBER OF SEQ ID NOS: 13
 24 <170> SOFTWARE: PatentIn version 3.3
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 224
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Mumps virus
 31 <400> SEQUENCE: 1
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 34 1 5 10 15
 37 Gly Met Asn Val Ala Asn His Phe Leu Ser Ala Pro Ile Gln Gly Thr
 38 20 25 30
 41 Asn Ser Leu Ser Lys Ala Ser Ile Pro Gly Val Ala Pro Val Leu
 42 35 40 45
 45 Ile Gly Asn Pro Glu Gln Lys Asn Ile Gln His Pro Thr Ala Ser His
 46 50 55 60
 49 Gln Gly Ser Lys Ser Lys Gly Ser Gly Ser Gly Val Arg Ser Ile Ile
 50 65 70 75 80
 53 Val Pro Pro Ser Glu Ala Gly Asn Gly Gly Thr Gln Ile Pro Glu Pro
 54 85 90 95
 57 Leu Phe Ala Gln Thr Gly Gln Gly Gly Ile Val Thr Thr Val Tyr Gln
 58 100 105 110
 61 Asp Pro Thr Ile Gln Pro Thr Gly Ser Tyr Arg Ser Val Glu Leu Ala
 62 115 120 125
 65 Lys Ile Gly Lys Glu Arg Met Ile Asn Arg Phe Val Glu Lys Pro Arg
 66 130 135 140
 69 Thr Ser Thr Pro Val Thr Glu Phe Lys Arg Gly Ala Gly Ser Gly Cys
 70 145 150 155 160
 73 Ser Arg Pro Asp Asn Pro Arg Gly Gly His Arg Arg Glu Trp Ser Leu
 74 165 170 175
 77 Ser Trp Val Gln Gly Glu Val Arg Val Phe Glu Trp Cys Asn Pro Ile

Cpg-6)

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78          180          185          190
81 Cys Ser Pro Ile Thr Ala Ala Ala Arg Phe His Ser Cys Lys Cys Gly
82          195          200          205
85 Asn Cys Pro Ala Lys Cys Asp Gln Cys Glu Arg Asp Tyr Gly Pro Pro
86          210          215          220
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90 <211> LENGTH: 675
91 <212> TYPE: DNA
92 <213> ORGANISM: Mumps virus
94 <400> SEQUENCE: 2
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97 gcaaatcatt tcctatccgc cccattccag ggaaccaact cgctgagcaa ggcctcaatc      120
99 atccctggcg ttgcacctgt actcattggc aatccagagc aaaagaacat tcagcaccct      180
101 accgcatcac atcagggatc caagtcaaag ggcagcggct caggggtcag gtccatcata      240
103 gtcccaccct ccgaagcagg caatggaggg actcagattc ctgagcccct ttttgacaaa      300
105 acaggacagg gtggtatagt caccacagtt tatcaggatc caactatcca accaacaggt      360
107 tcataaccgaa gtgtggaatt ggcgaagatc ggaaaagaga gaatgattaa tcgatttggt      420
109 gagaaaccta gaacctcaac gccggtgaca gaatttaaga ggggggccgg gagcggctgc      480
111 tcaaggccag acaatccaag aggagggcat agacgggaat ggagcctcag ctgggtccaa      540
113 ggagaggtcc gggctcttga gtggtgcaac cctatatgct cacctatcac tgccgcagca      600
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121 <211> LENGTH: 770
122 <212> TYPE: PRT
123 <213> ORGANISM: Homo sapiens
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132          20          25          30
135 Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser
136          35          40          45
139 Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile
140          50          55          60
143 Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln
144 65          70          75          80
147 His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu
148          85          90          95
151 Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu
152          100         105         110
155 Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln
156          115         120         125
159 Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu
160          130         135         140
163 Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln
164 145         150         155         160
167 Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr
168          165         170         175

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175 Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
176      195      200      205
179 Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
180      210      215      220
183 Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
184 225      230      235      240
187 Ala Asp Trp Lys Arg Arg Gln Gln Ile Ala Cys Ile Gly Gly Pro Pro
188      245      250      255
191 Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
192      260      265      270
195 Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
196      275      280      285
199 Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
200      290      295      300
203 Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
204 305      310      315      320
207 Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
208      325      330      335
211 Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
212      340      345      350
215 Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile
216      355      360      365
219 Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe
220      370      375      380
223 Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn
224 385      390      395      400
227 Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln
228      405      410      415
231 Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val
232      420      425      430
235 Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln
236      435      440      445
239 Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile
240      450      455      460
243 Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr
244 465      470      475      480
247 Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro
248      485      490      495
251 Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
252      500      505      510
255 Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
256      515      520      525
259 Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
260      530      535      540
263 Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
264 545      550      555      560
267 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile

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268          565          570          575
271 Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu
272          580          585          590
275 Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu
276          595          600          605
279 Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val
280          610          615          620
283 Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr
284 625          630          635          640
287 Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile Met Gly
288          645          650          655
291 Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr
292          660          665          670
295 Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg
296          675          680          685
299 Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro
300          690          695          700
303 Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn
304 705          710          715          720
307 Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln
308          725          730          735
311 Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe
312          740          745          750
315 Glu Ser Leu Thr Phe Asp Met Glu Leu Thr Ser Glu Cys Ala Thr Ser
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319 Pro Met
320          770
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324 <211> LENGTH: 3455
325 <212> TYPE: DNA
326 <213> ORGANISM: Homo sapiens
328 <400> SEQUENCE: 4
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331 ccgaggggaac aagccccaac cggatcctgg acaggcaccc cggcttggcg ctgtctctcc      120
333 ccctcggctc ggagaggccc ttcggcctga gggagcctcg ccgcccgtcc ccggcacacg      180
335 cgcagccccg gcctctcggc ctctgccgga gaaacagttg ggacccctga ttttagcagg      240
337 atggcccaat ggaatcagct acagcagctt gacacacggt acctggagca gctccatcag      300
339 ctctacagtg acagcttccc aatggagctg cggcagtttc tggccccttg gattgagagt      360
341 caagattggg catatgcggc cagcaaagaa tcacatgcca ctttggtggt tcataatctc      420
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349 actgcggccc agcaaggggg ccaggccaac caccacacag cagccgtggt gacggagaag      660
351 cagcagatgc tggagcagca ccttcaggat gtccggaaga gagtgcagga tctagaacag      720
353 aaaatgaaag tggtagagaa tctccaggat gactttgatt tcaactataa aaccctcaag      780
355 agtcaaggag acatgcaaga tctgaatgga aacaaccagt cagtgaccag gcagaagatg      840
357 cagcagctgg aacagatgct cactgcgctg gaccagatgc ggagaagcat cgtgagtgag      900
359 ctggcggggc ttttgtcagc gatggagtac gtgcagaaaa ctctcacgga cgaggagctg      960
361 gctgactgga agaggcgga acagattgcc tgcattggag gcccgcctaa catctgccta     1020

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363 gatcgggctag aaaactggat aacgtcatta gcagaatctc aacttcagac ccgtcaacaa 1080
365 attaagaaac tggaggagtt gcagcaaaaa gtttcctaca aaggggaccc cattgtacag 1140
367 caccggccga tgctggagga gagaatcgtg gagctgttta gaaacttaat gaaaagtgcc 1200
369 tttgtggtgg agcggcagcc ctgcatgccc atgcatcctg accggccccct cgtcatcaag 1260
371 accggcgctcc agttcactac taaagtcagg ttgctgggtca aattccctga gttgaattat 1320
373 cagcttaaaa ttaagtggtg cattgacaaa gactctgggg acgttgagc tctcagagga 1380
375 tcccggaaat ttaacattct gggcacaaa acaaaagtga tgaacatgga agaatccaac 1440
377 aacggcagcc tctctgcaga attcaaacac ttgaccctga gggagcagag atgtgggaat 1500
379 gggggccgag ccaattgtga tgcttccttg attgtgactg aggagctgca cctgatcacc 1560
381 tttgagaccg aggtgtatca ccaaggcctc aagattgacc tagagaccca ctcttgcca 1620
383 gttgtggtga tctccaacat ctgtcagatg ccaaatgcct gggcgctccat cctgtggtac 1680
385 aacatgctga ccaacaatcc caagaatgta aactttttta ccaagccccc aattggaacc 1740
387 tgggatcaag tggccgaggt cctgagctgg cagttctcct ccaccaccaa gcgaggactg 1800
389 agcatcgagc agctgactac actggcagag aaactcttgg gacctggtgt gaattattca 1860
391 ggggtgtcaga tcacatgggc taaattttgc aaagaaaaca tggtggcaa gggcttctcc 1920
393 ttctgggtct ggctggacaa tatcattgac cttgtgaaaa agtacatcct ggccctttgg 1980
395 aacgaagggt acatcatggg ctttatcagt aaggagcggg agcgggccat cttgagcact 2040
397 aagcctccag gcaccttctt gctaagattc agtgaaagca gcaaagaagg aggcgtcact 2100
399 ttcacttggg tggagaagga catcagcggg aagaccaga tccagtcctg ggaaccatac 2160
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421 taaatgcaaa taaggatgtg ttctctgaga cccatgatca ggggatgtgg cgggggggtg 2820
423 ctagaggagg aaaaaggaaa tgtcttgtgt tgttttgttc ccctgccctc ctttctcagc 2880
425 agctttttgt tattgttgtt gttgttctta gacaagtgcc tcctggtgcc tggggcatcc 2940
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429 gcacttttta accttgctga catccaaata gaagatagga ctatctaagc cctagggttc 3060
431 tttttaaatt aagaaataat aacaattaaa gggcaaaaaa cactgtatca gcatagcctt 3120
433 tctgtattta agaaacttaa gcagccgggc atggtggctc acgcctgtaa tcccagcact 3180
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439 tcccagctac tcgggaggct gaggcaggag aatcgcttga acctgagagg cggaggttgc 3360
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443 tgtctcaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 3455

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446 <210> SEQ ID NO: 5

447 <211> LENGTH: 750

448 <212> TYPE: PRT

449 <213> ORGANISM: Homo sapiens

451 <400> SEQUENCE: 5

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454 1 5 10 15

457 Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 1,2,3,4,5,7,8,9,11,12,13,14,15,16,17,18,19,20,21,22,24,25
Seq#:8; Xaa Pos. 26,28,29,30,31,32
Seq#:9; Xaa Pos. 7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26
Seq#:10; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:10; Xaa Pos. 24,26,27,28,29
Seq#:11; Xaa Pos. 7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26
Seq#:12; Xaa Pos. 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28
Seq#:12; Xaa Pos. 29

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12

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L:837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
M:341 Repeated in SeqNo=8
L:862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
M:341 Repeated in SeqNo=10
L:926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
M:341 Repeated in SeqNo=12